WHAT IS CLAIMED IS:

1. A method for preparing amplification products useful for forming an array of polynucleotides that is representative of a plurality of first polynucleotides comprising:

a) providing a plurality of samples of double-stranded polynucleotide fragments, wherein each sample is derived from a first polynucleotide;

b) ligating adapters to each end of the polynucleotide fragments to produce modified polynucleotide fragments, wherein each adapter comprises a first strand and a second strand, the second strand having a region of substantial complementarity to a region of the first strand;

c) amplifying the modified polynucleotide fragments to produce an amplification product for each sample of polynucleotide fragments;

d) isolating each amplification product; and

e) resuspending each amplification product to form a target solution suitable for application to a substrate to produce an array of polynucleotides.

2. The method of Claim 1 additionally comprising applying the target solutions to one or more substrates, wherein each target solution is applied to a distinct location on one substrate and/or target solutions are applied to different substrates that are combined to produce an array of polynucleotides.

3. The method of Claim 1 wherein the double-stranded polynucleotide fragments are derived from a polynucleotide library.

4. The method of Claim 3 wherein the polynucleotide library is a genomic DNA library.

5. The method of Claim 3 wherein the polynucleotide library is a cDNA library.

6. The method of Claim 3 wherein the double-stranded polynucleotide fragments are derived from YAC, BAC, P1 or PAC clones.

7. The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 50 kilobases.

8. The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 100 kilobases.

9. The method of Claim 7 wherein the first polynucleotides each have a complexity of less than about 500 kilobases.

10. The method of Claim 1 wherein the double-stranded polynucleotide fragments are obtained using one or more restriction endonucleases.

11. The method of Claim 1 wherein the average length of the double-stranded polynucleotide fragments is less than about 5 kilobases.

12. The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is less than about 2 kilobases.

13. The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is greater than about 100 basepairs.

14. The method of Claim 2 wherein the average volume of each target solution applied to the substrate is less than about 2 nanoliters.

15. The method of Claim 14 wherein the average volume of each target solution applied to the substrate is equal to greater than about 0.002 nanoliters.

16. The method of Claim 2 wherein the array comprises at least 1000 amplification products in a 1 cm^2 region of substrate.

17. The method of Claim 2 wherein the target solutions are robotically spotted on the substrate.

18. The method of Claim 2 wherein at least one strand of the adapters includes an amino group.

19. The method of Claim 1 wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume.

20. An array of polynucleotides that is representative of a plurality of first polynucleotides wherein said array is produced according to the method of Claim 2 and comprises at least 1000 amplification products in a 1 cm^2 region of substrate.

21. A plurality of target solutions prepared according to the method of Claim 3.

22. The plurality of target solutions of Claim 21 wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume.